

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical
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Application Serial Number: 10/593,798
Source: FWP
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IFWP

RAW SEQUENCE LISTING

DATE: 09/29/2006

PATENT APPLICATION: US/10/593,798

TIME: 09:07:26

Input Set : A:\01-SQ Listing-15 Sep 2006.txt

Output Set: N:\CRF4\09292006\J593798.raw

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3 <110> APPLICANT: Nielsen, Allan Kent
4      Rasmussen, Michael Dolberg
6 <120> TITLE OF INVENTION: Mutated prokaryotic cells with high secretion-levels
8 <130> FILE REFERENCE: 10576.204-US
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/593,798
C--> 10 <141> CURRENT FILING DATE: 2006-09-20
10 <160> NUMBER OF SEQ ID NOS: 26
12 <170> SOFTWARE: PatentIn version 3.3
14 <210> SEQ ID NO: 1
15 <211> LENGTH: 843
16 <212> TYPE: DNA
17 <213> ORGANISM: Bacillus subtilis 168
19 <400> SEQUENCE: 1
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24 cagcttcgag aattggctgc agcacacaat gtgtctgatt ctattcacat tacagctctc      180
26 gatgtcaccg atgaacaatc tatagtctca ttcgaaaag ctgttagtgc ttacgccccg      240
28 atcgatttac tcgttaacaa cgccggaacg gcttatggag gatttatcga ggatgtgccg      300
30 atggaacatt tcagacaaca atttgaaacg aatgtcttcg gtgtgatcca tgtgacaaaa      360
32 accgtgctgc cttacataag aaagcatggc ggcgcaaaga ttataaacgt gagcagcatc      420
34 agcggactga caggattccc agcgtgtcgc ccatatgttt cttccaagca tgcattggaa      480
36 ggtttttctg aaagcctgcg tatcgagctg cttccgttcg gtatcgaaac cgctttgatc      540
38 gagccgggct catacaagac atcgatctgg tcaacgtcat tatcaaattt tatgtcggtg      600
40 cctgctgacg attcagccta tcatcaatac tataaaaaga tcctttccta tgttcaaaaa      660
42 aacggagaag aaagcggaga tccccaaag gttgccgacc tcatttatca attggcaaca      720
44 aaacagcaca taaagaattt gcgatacccg atcggaaagg gcatcaagct caccctgctg      780
46 ttccgatcgc tttttccttg gtctgcgtgg gagtctatcc tgaagaaaaa gctattcagc      840
48 tga
51 <210> SEQ ID NO: 2
52 <211> LENGTH: 280
53 <212> TYPE: PRT
54 <213> ORGANISM: Bacillus subtilis 168
56 <400> SEQUENCE: 2
58 Met Asn Lys Lys Ile Ala Ile Val Thr Gly Ala Ser Ser Gly Phe Gly
59 1          5          10          15
62 Leu Leu Ala Ala Val Lys Leu Ala Arg Ser Phe Phe Val Ile Ala Thr
63          20          25          30
66 Ser Arg Gln Pro Glu Lys Ala Glu Gln Leu Arg Glu Leu Ala Ala Ala
67          35          40          45
70 His Asn Val Ser Asp Ser Ile His Ile Thr Ala Leu Asp Val Thr Asp
71          50          55          60
74 Glu Gln Ser Ile Val Ser Phe Gly Lys Ala Val Ser Ala Tyr Ala Pro
75 65          70          75          80

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78 Ile Asp Leu Leu Val Asn Asn Ala Gly Thr Ala Tyr Gly Gly Phe Ile
79           85           90           95
82 Glu Asp Val Pro Met Glu His Phe Arg Gln Gln Phe Glu Thr Asn Val
83           100           105           110
86 Phe Gly Val Ile His Val Thr Lys Thr Val Leu Pro Tyr Ile Arg Lys
87           115           120           125
90 His Gly Gly Ala Lys Ile Ile Asn Val Ser Ser Ile Ser Gly Leu Thr
91           130           135           140
94 Gly Phe Pro Ala Leu Ser Pro Tyr Val Ser Ser Lys His Ala Leu Glu
95 145           150           155           160
98 Gly Phe Ser Glu Ser Leu Arg Ile Glu Leu Leu Pro Phe Gly Ile Glu
99           165           170           175
102 Thr Ala Leu Ile Glu Pro Gly Ser Tyr Lys Thr Ser Ile Trp Ser Thr
103           180           185           190
106 Ser Leu Ser Asn Phe Met Ser Val Pro Ala Asp Asp Ser Ala Tyr His
107           195           200           205
110 Gln Tyr Tyr Lys Lys Ile Leu Ser Tyr Val Gln Lys Asn Gly Glu Glu
111           210           215           220
114 Ser Gly Asp Pro Gln Glu Val Ala Asp Leu Ile Tyr Gln Leu Ala Thr
115 225           230           235           240
118 Lys Gln His Ile Lys Asn Leu Arg Tyr Pro Ile Gly Lys Gly Ile Lys
119           245           250           255
122 Leu Thr Leu Leu Phe Arg Ser Leu Phe Pro Trp Ser Ala Trp Glu Ser
123           260           265           270
126 Ile Leu Lys Lys Lys Leu Phe Ser
127           275           280
130 <210> SEQ ID NO: 3
131 <211> LENGTH: 1503
132 <212> TYPE: DNA
133 <213> ORGANISM: Bacillus subtilis 168
135 <400> SEQUENCE: 3
136 atgaatcggc tttccgcaga ttttcaatcg tcgctcggtta cattagatca taaacttggtg      60
138 gacattaatc aagacgtgtg gaatgaattg ttaacaaaac cgggattgcg cgatgtttct      120
140 tacatattaa atgaaagaag acagagggtt gccgaaaagc ttagccccgg taaggaaaaa      180
142 ctgatcggaa accttgcggt ggacggatat cacgcttgga gtgacttata caatatgggt      240
144 gtcgggaaaa tgacgatccc gtatgaggaa aacggtgaaa acaagcaatt gtctgtcggt      300
146 caggcgagaa atatgatgga tcatcaagac cgtactgtca gaaaaacagt atatgaacgt      360
148 ttccgccaag cttgggagag caagcaagat attttcagca gcacgctgaa tcatttggcg      420
150 ggattccggc ttgaaaccta taaagcgcgc ggctgggaga atgtcctgaa ggaaccgctg      480
152 caaattaaca ggatgaaaaa agaaacactt gatacgatgt ggcaggatcat cactgaaaac      540
154 aagaagccgt tcgttcagtt tttgaaccgg aaagcatcca tgctcggcct tgaaaaactc      600
156 agctggttac atgtcgaggc accgatcggt tctgacggaa aggtctattc gtatgatgaa      660
158 gccgcaaata tcattaccag ccagttttca acgtttggca aaaagctgtc ctcattcact      720
160 gaaaaagcgt ttcgggacgg ctggattgag gcggaagaca ggagcggaaa aagagtcggc      780
162 ggcttttgca ccagttttcc ggacagcggg gaatcccgga ttttcatgac attttcggga      840
164 agcgctcaa atgtctctac ccttgcgcat gaactcgggc acgcgttcca tcaggaagca      900
166 atgctcaacg tcaggccggt aaaccgttcc tacgccatga acgttgacaga aacagcttca      960
168 acgtttgcag agatgatagt ggcggacgcg actgtccagc aggccgagac gagggaagaa     1020
170 aagcttggtc ttctggagga taaagtgcaa agaagcgttg cgttcttcat gaacattcac     1080

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172 gcaagatttc tatttgaac gagattctac gaggaacgaa agcggggagt ggtaccggcc 1140
174 agccgcttga atgagctgat ggaagaggcg caaagagagg catactgcaa tgcgttagaa 1200
176 gaatatcatc cgcttttttg ggcatacaag cttcattttc acatcacgag ggtgccggtt 1260
178 tacaatttcc cttatacatt cggctacctg ttttctcttg gtatttacgc gttggcgctt 1320
180 gaagaaaaag acacattcga agagaagtat atggcgctat tgcgcgatac ggcttctatg 1380
182 acagtggagg atttggcgat gaagcatttg ggcgctgaca tcacaaagcg cgatttctgg 1440
184 gagaatgcca tcaagctggc tgtgcgtgac gccgaaacct ttttacaaat gaccgaatct 1500
186 taa 1503
189 <210> SEQ ID NO: 4
190 <211> LENGTH: 500
191 <212> TYPE: PRT
192 <213> ORGANISM: Bacillus subtilis 168
194 <400> SEQUENCE: 4
196 Met Asn Arg Leu Ser Ala Asp Phe Gln Ser Ser Leu Val Thr Leu Asp
197 1 5 10 15
200 His Lys Leu Val Asp Ile Asn Gln Asp Val Trp Asn Glu Leu Leu Thr
201 20 25 30
204 Lys Pro Gly Leu Arg Asp Val Ser Tyr Ile Leu Asn Glu Arg Arg Gln
205 35 40 45
208 Arg Val Ala Glu Lys Leu Ser Pro Gly Lys Glu Lys Leu Ile Gly Asn
209 50 55 60
212 Leu Ala Val Asp Gly Tyr His Ala Trp Ser Asp Leu Tyr Asn Met Val
213 65 70 75 80
216 Val Gly Lys Met Thr Ile Pro Tyr Glu Glu Asn Gly Glu Asn Lys Gln
217 85 90 95
220 Leu Ser Val Gly Gln Ala Glu Asn Met Met Asp His Gln Asp Arg Thr
221 100 105 110
224 Val Arg Lys Thr Val Tyr Glu Arg Phe Arg Gln Ala Trp Glu Ser Lys
225 115 120 125
228 Gln Asp Ile Phe Ser Ser Thr Leu Asn His Leu Ala Gly Phe Arg Leu
229 130 135 140
232 Glu Thr Tyr Lys Ala Arg Gly Trp Glu Asn Val Leu Lys Glu Pro Leu
233 145 150 155 160
236 Gln Ile Asn Arg Met Lys Lys Glu Thr Leu Asp Thr Met Trp Gln Val
237 165 170 175
240 Ile Thr Glu Asn Lys Lys Pro Phe Val Gln Phe Leu Asn Arg Lys Ala
241 180 185 190
244 Ser Met Leu Gly Leu Glu Lys Leu Ser Trp Tyr Asp Val Glu Ala Pro
245 195 200 205
248 Ile Gly Ser Asp Gly Lys Val Tyr Ser Tyr Asp Glu Ala Ala Asn Ile
249 210 215 220
252 Ile Thr Ser Gln Phe Ser Thr Phe Gly Lys Lys Leu Ser Ser Phe Thr
253 225 230 235 240
256 Glu Lys Ala Phe Arg Asp Gly Trp Ile Glu Ala Glu Asp Arg Ser Gly
257 245 250 255
260 Lys Arg Val Gly Gly Phe Cys Thr Ser Phe Pro Asp Ser Gly Glu Ser
261 260 265 270
264 Arg Ile Phe Met Thr Phe Ser Gly Ser Ala Ser Asn Val Ser Thr Leu
265 275 280 285

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268 Ala His Glu Leu Gly His Ala Phe His Gln Glu Ala Met Leu Asn Val
269      290                      295                      300
272 Arg Pro Leu Asn Arg Ser Tyr Ala Met Asn Val Ala Glu Thr Ala Ser
273 305                      310                      315                      320
276 Thr Phe Ala Glu Met Ile Val Ala Asp Ala Thr Val Gln Gln Ala Glu
277      325                      330                      335
280 Thr Arg Glu Glu Lys Leu Val Leu Leu Glu Asp Lys Val Gln Arg Ser
281      340                      345                      350
284 Val Ala Phe Phe Met Asn Ile His Ala Arg Phe Leu Phe Glu Thr Arg
285      355                      360                      365
288 Phe Tyr Glu Glu Arg Lys Arg Gly Val Val Pro Ala Ser Arg Leu Asn
289      370                      375                      380
292 Glu Leu Met Glu Glu Ala Gln Arg Glu Ala Tyr Cys Asn Ala Leu Glu
293 385                      390                      395                      400
296 Glu Tyr His Pro Leu Phe Trp Ala Ser Lys Leu His Phe His Ile Thr
297      405                      410                      415
300 Arg Val Pro Phe Tyr Asn Phe Pro Tyr Thr Phe Gly Tyr Leu Phe Ser
301      420                      425                      430
304 Leu Gly Ile Tyr Ala Leu Ala Leu Glu Glu Lys Asp Thr Phe Glu Glu
305      435                      440                      445
308 Lys Tyr Met Ala Leu Leu Arg Asp Thr Ala Ser Met Thr Val Glu Asp
309      450                      455                      460
312 Leu Ala Met Lys His Leu Gly Ala Asp Ile Thr Lys Arg Asp Phe Trp
313 465                      470                      475                      480
316 Glu Asn Ala Ile Lys Leu Ala Val Arg Asp Ala Glu Thr Phe Leu Gln
317      485                      490                      495
320 Met Thr Glu Ser
321      500
324 <210> SEQ ID NO: 5
325 <211> LENGTH: 297
326 <212> TYPE: DNA
327 <213> ORGANISM: Bacillus subtilis 168
329 <400> SEQUENCE: 5
330 atggcgctgc aaggggtagg ccaaagatgg gatcttgatt cattttttaaa gggcgggagc      60
332 caatcggaag aattcaaagg ttatattgag aagctgtcac aaagtctgcg tgcatttcaa      120
334 gacaggactg atgcgtttca ggtgcctgaa tcgcctgaag aggctgaagg gctgaccgcg      180
336 ttgcttgatt taatcgaaca gacatccgtc aagcttcagc aggccggcgc ttttgttgct      240
338 tgcctccagg cccagaatat caatgatcaa aaggctatag agcatcaggc ctcatga      297
341 <210> SEQ ID NO: 6
342 <211> LENGTH: 98
343 <212> TYPE: PRT
344 <213> ORGANISM: Bacillus subtilis 168
346 <400> SEQUENCE: 6
348 Met Ala Leu Gln Gly Val Gly Gln Arg Trp Asp Leu Asp Ser Phe Phe
349 1                      5                      10                      15
352 Lys Gly Gly Ser Gln Ser Glu Glu Phe Lys Gly Tyr Ile Glu Lys Leu
353      20                      25                      30
356 Ser Gln Ser Leu Arg Ala Phe Gln Asp Arg Thr Asp Ala Phe Gln Val
357      35                      40                      45

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360 Pro Glu Ser Pro Glu Glu Ala Glu Gly Leu Thr Ala Leu Leu Asp Leu
361      50                      55                      60
364 Ile Glu Gln Thr Ser Val Lys Leu Gln Gln Ala Gly Ala Phe Val Ala
365 65                      70                      75                      80
368 Cys Leu Gln Ala Gln Asn Ile Asn Asp Gln Lys Ala Ile Glu His Gln
369                      85                      90                      95
372 Ala Ser
376 <210> SEQ ID NO: 7
377 <211> LENGTH: 25
378 <212> TYPE: DNA
379 <213> ORGANISM: artificial sequence
381 <220> FEATURE:
382 <223> OTHER INFORMATION: Primer yusZ1F
384 <400> SEQUENCE: 7
385 ccttcccggg gctaagcttt tcggc                                25
388 <210> SEQ ID NO: 8
389 <211> LENGTH: 30
390 <212> TYPE: DNA
391 <213> ORGANISM: artificial sequence
393 <220> FEATURE:
394 <223> OTHER INFORMATION: Primer yusZ2R
396 <400> SEQUENCE: 8
397 gatagactcc cacgcgctgg acgctcctgt                                30
400 <210> SEQ ID NO: 9
401 <211> LENGTH: 30
402 <212> TYPE: DNA
403 <213> ORGANISM: artificial sequence
405 <220> FEATURE:
406 <223> OTHER INFORMATION: Primer yusZ2F
408 <400> SEQUENCE: 9
409 acaggagcgt ccagcgcggtg ggagtctatc                                30
412 <210> SEQ ID NO: 10
413 <211> LENGTH: 25
414 <212> TYPE: DNA
415 <213> ORGANISM: artificial sequence
417 <220> FEATURE:
418 <223> OTHER INFORMATION: Primer yusZ3R
420 <400> SEQUENCE: 10
421 aacggtaccc tgaccaagca gacag                                25
424 <210> SEQ ID NO: 11
425 <211> LENGTH: 25
426 <212> TYPE: DNA
427 <213> ORGANISM: artificial sequence
429 <220> FEATURE:
430 <223> OTHER INFORMATION: Primer yusX1F
432 <400> SEQUENCE: 11
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436 <210> SEQ ID NO: 12
437 <211> LENGTH: 30

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VERIFICATION SUMMARY

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L:10 M:270 C: Current Application Number differs, Replaced Current Application No

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date